



# **Expression and Characterization of a Novel Cold-Adapted Chitosanase from Marine** *Renibacterium* **sp. Suitable for Chitooligosaccharides Preparation**

Lin-Lin Zhang <sup>1</sup>, Xiao-Hua Jiang <sup>2</sup>, Xin-Feng Xiao <sup>1</sup>, Wen-Xiu Zhang <sup>1</sup>, Yi-Qian Shi <sup>1</sup>, Zhi-Peng Wang <sup>3,\*</sup> and Hai-Xiang Zhou <sup>2,\*</sup>

- <sup>1</sup> College of Safety and Environmental Engineering, Shandong University of Science and Technology, Qingdao 266510, China; linlinzhsd@126.com (L.-L.Z.); xf.xiao@163.com (X.-F.X.); zhangwx19991@163.com (W.-X.Z.); Shiyiqian0715@163.com (Y.-Q.S.)
- <sup>2</sup> Tobacco Research Institute, Chinese Academy of Agricultural Sciences, Qingdao 266101, China; xiaohuaaoe@163.com
- <sup>3</sup> Marine Science and Engineering College, Qingdao Agricultural University, Qingdao 266109, China
- \* Correspondence: wangzpmbio@163.com (Z.-P.W.); pro.zhouhaixiang@163.com (H.-X.Z.)

check for updates

Article

Citation: Zhang, L.-L.; Jiang, X.-H.; Xiao, X.-F.; Zhang, W.-X.; Shi, Y.-Q.; Wang, Z.-P.; Zhou, H.-X. Expression and Characterization of a Novel Cold-Adapted Chitosanase from Marine *Renibacterium* sp. Suitable for Chitooligosaccharides Preparation. *Mar. Drugs* 2021, *19*, 596. https:// doi.org/10.3390/md19110596

Academic Editors: Jessica Amber Jennings and Bill J. Baker

Received: 11 September 2021 Accepted: 19 October 2021 Published: 21 October 2021

**Publisher's Note:** MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



**Copyright:** © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). Abstract: (1) Background: Chitooligosaccharides (COS) have numerous applications due to their excellent properties. Chitosan hydrolysis using chitosanases has been proposed as an advisable method for COS preparation. Although many chitosanases from various sources have been identified, the cold-adapted ones with high stability are still rather rare but required. (2) Methods: A novel chitosanase named CsnY from marine bacterium Renibacterium sp. Y82 was expressed in Escherichia coli, following sequence analysis. Then, the characterizations of recombinant CsnY purified through Ni–NTA affinity chromatography were conducted, including effects of pH and temperature, effects of metal ions and chemicals, and final product analysis. (3) Results: The GH46 family chitosanase CsnY possessed promising thermostability at broad temperature range (0-50 °C), and with optimal activity at 40 °C and pH 6.0, especially showing relatively high activity (over 80% of its maximum activity) at low temperatures (20-30 °C), which demonstrated the cold-adapted property. Common metal ions or chemicals had no obvious effect on CsnY except Mn<sup>2+</sup> and Co<sup>2+</sup>. Finally, CsnY was determined to be an endo-type chitosanase generating chitodisaccharides and -trisaccharides as main products, whose total concentration reached 56.74 mM within 2 h against 2% (w/v) initial chitosan substrate. (4) Conclusions: The results suggest the cold-adapted CsnY with favorable stability has desirable potential for the industrial production of COS.

Keywords: chitosanase; cold adaptation; chitooligosaccharide; Renibacterium sp.

# 1. Introduction

Chitooligosaccharides (COS) are the hydrolytic products of the chitosan derived from the total or partial deacetylation of chitin which is the second-most ubiquitous polysaccharide in nature. COS have attracted much attention in recent years because of their versatile pharmacological activities and biological functions, thus applicability in various fields, such as antioxidant activity [1], anti-inflammatory activity [2], immunomodulation [3,4], cosmetic industry [5], agricultural industry [6,7], and so on. COS can be prepared by physical, chemical, and enzymatic degradation methods. However, chemical production of COS is environmentally hazardous and generally difficult to produce specific COS, always accompanied by the generation of mixed oligosaccharides with varying degrees of polymerization (DPs) [7]. Therefore, environmentally compatible and reproducible alternatives for preparation of COS are desirable. Enzymatic method is an excellent alternative to conventional processes, which can yield better-defined COS or degraded chitosan with desired physicochemical and biological properties [8].

The enzymes for the depolymerization of chitosan include the specific enzymes called chitosanases and some non-specific enzymes, such as carbohydrases and proteases [9]. As a type of glycoside hydrolase, chitosanase (EC 3.2.1.132) catalyzes the hydrolysis of  $\beta$ -1,4-linked glycosidic bond of chitosan and release COS as major product. According to the carbohydrate-active enzymes (CAZy) database, chitosanases can be grouped into several different glycoside hydrolyase (GH) families, among which GH46, 75, and 80 families contain chitosanases exclusively [10]. Most reported chitosanases belong to GH46; the members of this family have been characterized most extensively and have a highly electronegative substrate-binding cleft compared with other chitosanases [10]. Thus far, chitosanases have been found in many organisms including bacteria, fungi, plants, and viruses [11]. Most of these characterized chitosanases come from the terrestrial environment; only a few reports referred to the marine-derived chitosanases [11]. Marine microorganisms are endowed with unique genetic structures by the marine environment, and as a result are considered as new promising sources of the enzymes with unsuspected application potential [11]. For example, a GH46 chitosanase CsnA identified from Renibacterium sp. QD1 from the coast of Qingdao, China, displayed a broad pH stability of 5.0–10.0 [12]. An endo-type chitosanase CHIS5 mined from the metagenome of marine microorganisms has been used to degrade acetylated chitosan for efficient production of COS associating with the chitin deacetylase CDA20 [13].

To date, a variety of chitosanases have been identified; nevertheless the enzymes with special properties, such as cold-adaption, thermo-tolerance and single product distribution, are still few but required for industrial production [14]. In the past few years, some of the cold-adapted chitosanase-producing microorganisms have been isolated, such as *Bacillus* sp. BY01 and *Pseudoalteromonas* sp. SY39 [15,16]. Cold-adapted enzymes show high relative catalytic activities at low temperatures (generally less than 30 °C); even the optimal temperature may be higher [17]. Compared with the mesophilic enzymes, cold-adapted ones have evolved a range of structural features with high level of flexibility, which confer strong adaptation at low temperatures onto the enzymes [16,17]. These characteristics make running enzymatic processes possible at room or even lower temperatures without heating, which are conducive to reducing energy costs and contamination risks, and enhancing reaction process controllability in industrial production [18,19]. Therefore, cold-adapted enzymes have been found to be attractive in bioconversion.

Herein, a new cold-adapted chitosanase CsnY from the marine bacterium *Renibacterium* sp. Y82 was purified and characterized after heterologous expression by *Escherichia coli*. CsnY was identified as an endo-type chitosanase by hydrolytic products analysis and also had excellent thermo-tolerance properties. Noticeably, further biochemical characterization showed that almost all common metal ions or chelators had no obvious influence on the enzymatic activity of CsnY. These properties of CsnY suggest it could be regarded as excellent potential candidate for industrial applications of COS production.

#### 2. Results

#### 2.1. CsnY Sequence Analysis

In previous work, the marine bacterium *Renibacterium* sp. Y82 displayed the ability to degrade chitosan and grow in a chitosan sole-carbon medium (detailed data not shown). The genomic analysis of Y82 implied there existed a putative chitosanase-encoding gene *csnY* (Genbank number MT741946), the ORF of which consisted of 945 bp, encoding 314 amino acids with a signal peptide of 60 amino acids (Met<sup>1</sup>–Ala<sup>60</sup>) in the N-terminal (Figure 1). The amino acid sequence analysis based on the Conserved Domain Database (CDD) from the National Center of Biotechnology Information (NCBI, Bethesda, MD, USA) showed that CsnY had a conserved domain feature as a lysozyme-like superfamily of chitosanase-glyco-hydro-46 site, marked with a black line in Figure 1. Therefore, CsnY was determined as a member of the GH46 family, which is further classified into five different clusters from A to E. The phylogenic analysis result displayed CsnY was affiliated to Cluster A and originated from the same ancestral node with the chitosanase from *Renibacterium* 

*salmoninarum* (Genbank number WP\_041684833.1) (Figure 2). The mature enzyme of CsnY protein had a calculated Mw of 27.8 kDa and pI value of 5.98. Multiple sequences alignment among CsnY and other typical chitosanase proteins of Cluster A indicated that CsnY shared 60.65% amino acid identity.



**Figure 1.** Multiple sequences alignment among CsnY and other related chitosanases of GH46 family. AMED\_6991 (GenBank number: ADJ48710.1), AORI\_1736 (GenBank number: AGM04324.1), chitosanase (GenBank number: WP\_15853930.1), RSal33209\_3139 (GenBank number: ABY24857.1), CsnN174 (GenBank number: AAA19865.1), CsnY (GenBank number: MT741946). The signal peptide was underlined with red dotted line. The key residues for catalysis and stabilization were labeled with a green star. The conserved sequence with the characteristic of lysozyme-like superfamily was marked with a black line.



Figure 2. Phylogenetic analysis of CsnY and other chitosanases which belong to GH46.

## 2.2. Expression and Purification of CsnY

The *csnY* nucleotide sequence was optimized without the signal sequence and shown in Figure 3. Heterologous expression of CsnY fused with  $6 \times$ His-tag in the C-terminal was performed in *E. coli* BL21 (DE3). After 20 h of IPTG induction, the recombinant CsnY was

purified via Ni–NTA affinity chromatography and finally the activity reached 369.31 U/mL after concentration through ultrafiltration, with a specific activity of 330.67 U/mg. The recombinant CsnY showed a single band located in SDS-PAGE gel with around 30 kDa (Figure 4), which was a little higher than the deduced Mw (27.8 kDa) of the mature enzyme, on account of fusing with  $6 \times$ His-tag and addition of the restriction sites to the ends of the gene for construction of the plasmid, which introduced 10 extra amino acids into recombinant CsnY.

Original	1	AAC	GCA	GTA	TCC	TCT	TTA	GCC	CCA	GCA	ATC	ACG	GCA	GTT	TCG	GCC	GCA	AGC	ACG	GGC	GAC
Optimized	1	AAT	GCA	GTT	AGC	AGC	CTG	GCA	CCG	GCA	ATT	ACC	GCA	GTG	AGT	GCC	GCA	AGC	ACC	GGT	GAC
Amino acid	1	Ν	Α	v	S	S	L	Α	Р	Α	Ι	Т	Α	V	S	Α	Α	S	Т	G	D
Original	61	CTG	TCC	GCT	CCG	GCC	AAA	AAG	GAA	ATC	GCG	ATG	CAA	CTT	GTG	TGC	AGC	GCA	GAA	AAC	TCC
Optimized	61	CTG	AGC	GCA	CCG	GCC	AAA	AAA	GAA	ATT	GCA	ATG	CAG	CTG	GTG	TGC	AGC	GCA	GAA	AAT	AGC
Amino acid	21	L	S	Α	Р	Α	K	K	Е	I	Α	М	Q	L	v	С	S	Α	Е	Ν	S
Original	121	TCC	CTA	GAT	TGG	AAA	GCC	CAG	TAC	GGC	TAC	ATC	GAA	GAC	ATC	GAT	GAC	GAC	CGC	GGC	TAC
Optimized	121	AGC	CTG	GAT	TGG	AAA	GCC	CAG	TAT	GGC	TAT	ATT	GAA	GAT	ATT	GAT	GAT	GAC	CGT	GGT	TAT
Amino acid	41	S	L	D	W	K	Α	Q	Y	G	Y	I	Е	D	I	D	D	D	R	G	Y
Original	181	ACC	GGA	GGC	ATA	ATC	GGC	TTC	ACC	TCG	GGC	ACC	GGA	GAC	ATG	CTC	GAG	CTG	GTG	CAA	AAC
Optimized	181	ACC	GGC	GGT	ATT	ATT	GGC	TTT	ACC	AGT	GGC	ACC	GGC	GAT	ATG	CTG	GAA	CTG	GTT	CAG	AAT
Amino acid	61	Т	G	G	I	I	G	F	Т	S	G	Т	G	D	М	L	E	L	v	Q	Ν
Original	241	TAT	GCA	AAT	ACC	AAG	CCA	GAC	AAC	AAC	GTC	CTC	AAG	CCT	TTC	CTG	CCG	GTA	CTC	CGC	AAA
Optimized	241	TAT	GCA	AAT	ACC	AAA	CCG	GAT	AAT	AAC	GTG	CTG	AAA	CCG	TTT	CTG	CCG	GTT	CTG	CGT	AAA
Amino acid	81	Y	Α	N	Т	K	Р	D	Ν	Ν	v	L	К	Р	F	L	Р	V	L	R	K
Original	301	GTC	AAC	GGC	ACA	AAA	TCT	CAC	GAA	GGA	CTG	GGC	CAG	AAA	TAC	GTT	GAC	GCT	TGG	CAT	CAG
Optimized	301	GTT	AAT	GGC	ACC	AAA	AGC	CAT	GAA	GGC	CTG	GGT	CAG	AAA	TAT	GTT	GAT	GCC	TGG	CAT	CAG
Amino acid	101	v	Ν	G	Т	К	S	Н	Е	G	L	G	Q	К	Y	v	D	Α	W	Н	Q
Original	361	GCA	GCT	AAA	GAC	TCC	GTG	TTC	CTC	AAG	GAA	CAA	GAC	AAA	TTG	CGA	GAC	AGT	ATG	TAT	TTC
Optimized	361	GCC	CCC	A A A	CAT	ACC	GTG	ттт	CTG	ΔΔΔ	GAA	CAG	GAT	AAA	СТС	ССТ	CAT	ACT	ATC	ТАТ	ттт
opermined	001	000	GCC	AAA	GAT	AUC	010		010	AAA	om	ono	0111	mm	010	0.01	GAT	AGI	AIG	IAI	
Amino acid	121	A	A	K	D	S	v	F	L	K	E	Q	D	K	L	R	D	S	M	Y	F
Amino acid Original	121 421	A AAC	A CCC	K GCG	D GTC	S AGC	V CAA	F GGT	L AAG	K TCG	E GAC	Q GGA	D TTG	K AGC	L AAT	R CTG	D GGT	S CAA	M TTC	Y ATG	F TAT
Amino acid Original Optimized	121 421 421	A AAC AAC	A CCC CCG	K GCG GCA	D GTC GTG	S AGC AGT	V CAA CAG	F GGT GGT	L AAG AAA	K TCG AGT	E GAC GAT	Q GGA GGT	D TTG CTG	K AGC AGT	L AAT AAT	R CTG CTG	D GGT GGT	S CAA CAG	M TTC TTT	Y ATG ATG	F TAT TAT
Amino acid Original Optimized Amino acid	121 421 421 141	A AAC AAC N	A CCC CCG P	K GCG GCA A	D GTC GTG V	S AGC AGT S	V CAA CAG Q	F GGT GGT G	L AAG AAA K	K TCG AGT S	E GAC GAT D	Q GGA GGT G	D TTG CTG L	K AGC AGT S	L AAT AAT N	R CTG CTG L	D GGT GGT G	S CAA CAG Q	M TTC TTT F	Y ATG ATG M	F TAT TAT Y
Amino acid Original Optimized Amino acid Original	121 421 421 141 481	A AAC AAC N TAC	A CCC CCG P GAC	K GCG GCA A GCA	D GTC GTG V ATT	S AGC AGT S TTC	V CAA CAG Q ATG	F GGT GGT G CAC	L AAG AAA K GGC	K TCG AGT S CCC	E GAC GAT D GGC	Q GGA GGT G GAC	D TTG CTG L TCA	K AGC AGT S TCC	L AAT AAT N GAC	R CTG CTG L TCC	D GGT GGT G TTC	S CAA CAG Q GGT	M TTC TTT F GGC	Y ATG ATG M ATC	F TAT TAT Y AGG
Amino acid Original Optimized Amino acid Original Optimized	121 421 421 141 481 481	A AAC AAC N TAC TAT	A CCC CCG P GAC GAT	K GCG GCA A GCA GCA	D GTC GTG V ATT ATT	S AGC AGT S TTC TTC	V CAA CAG Q ATG ATG	F GGT GGT G CAC CAC	L AAG AAA K GGC GGC	K TCG AGT S CCC CCG	E GAC GAT D GGC GGC	Q GGA GGT G GAC GAT	D TTG CTG L TCA	K AGC AGT S TCC AGT	L AAT AAT N GAC GAT	R CTG CTG L TCC AGC	D GGT GGT G TTC TTT	S CAA CAG Q GGT GGC	M TTC TTT F GGC GGT	Y ATG ATG M ATC ATT	F TAT TAT Y AGG CGC
Amino acid Original Optimized Amino acid Original Optimized Amino acid	121 421 421 141 481 481 161	A AAC AAC N TAC TAT Y	A CCCC CCG P GAC GAT D	K GCG GCA A GCA GCA GCA A	D GTC GTG V ATT ATT I	S AGC AGT S TTC TTC F	V CAA CAG Q ATG ATG M	F GGT GGT G CAC CAC H	L AAG AAA K GGC GGC G	K TCG AGT S CCC CCG P	E GAC GAT D GGC GGC G	Q GGA GGT GAC GAT D	D TTG CTG L TCA AGC S	K AGC AGT S TCC AGT S	L AAT AAT N GAC GAT D	R CTG CTG L TCC AGC S	D GGT GGT G TTC TTT F	S CAA CAG Q GGT GGC G	M TTC TTT F GGC GGT G	Y ATG ATG M ATC ATC I	F TAT TAT Y AGG CGC R
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original	121 421 421 141 481 481 161 541	A AAC AAC N TAC TAT Y AAA	A CCC P GAC GAT D TCG	K GCG GCA A GCA GCA A GCC	D GTC GTG V ATT ATT I ATG	S AGC AGT S TTC TTC F AAG	V CAA CAG Q ATG ATG M AAC	F GGT GGT G CAC CAC H GCG	L AAG AAA K GGC GGC G AAG	K TCG AGT S CCC CCG P ACA	E GAC GAT D GGC GGC G CCG	Q GGA GGT GAC GAT D GCG	D TTG CTG L TCA AGC S CAG	K AGC AGT S TCC AGT S GGT	L AAT AAT N GAC GAT D GGC	R CTG CTG L TCC AGC S GAC	D GGT GGT G TTC TTT F GAG	S CAA CAG Q GGT GGC G AAG	M TTC TTT F GGC GGT G ACC	Y ATG ATG M ATC ATT I TAT	F TAT TAT Y AGG CGC R CTG
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized	121 421 421 141 481 481 161 541 541	A AAC AAC N TAC TAT Y AAA AAA	A CCC P GAC GAT D TCG AGT	K GCG GCA A GCA GCA A GCC GCC	D GTC GTG V ATT ATT I ATG ATG	S AGC AGT S TTC TTC F AAG AAA	V CAA Q ATG ATG M AAC AAT	F GGT GGT G CAC CAC H GCG GCC	L AAG AAA K GGC GGC G AAG AAA	K TCG AGT S CCC CCG P ACA ACC	E GAC GAT D GGC GGC G CCG CCG	Q GGA GGT GAC GAT D GCG GCC	D TTG CTG L TCA AGC S CAG CAG	K AGC AGT S TCC AGT S GGT GGC	L AAT AAT N GAC GAT D GGC GGT	R CTG CTG L TCC AGC S GAC GAC	D GGT GGT TTC TTT F GAG GAA	S CAA CAG Q GGT GGC G AAG AAA	M TTC TTT F GGC GGT G ACC ACC	Y ATG ATG M ATC ATT I TAT TAT	F TAT TAT Y AGG CGC R CTG CTG
Amino acid Original Optimized Amino acid Optimized Amino acid Original Optimized Amino acid	121 421 421 141 481 481 161 541 541 181	A AAC AAC N TAC TAT Y AAA AAA K	A CCC CCG P GAC GAT D TCG AGT S	K GCG GCA A GCA GCA A GCC GCC GCC A	D GTC GTG V ATT ATT I ATG ATG M	S AGC AGT S TTC TTC F AAG AAA K	V CAA CAG Q ATG ATG ATG M AAC AAT N	F GGT GGT CAC CAC CAC H GCG GCC A	L AAG AAA K GGC GGC G AAG AAA K	K TCG AGT S CCC CCG P ACA ACC T	E GAC GAT D GGC GGC GGC CCG CCG P	Q GGA GGT GAC GAT D GCG GCC A	D TTG CTG L TCA AGC S CAG CAG Q	K AGC AGT S TCC AGT S GGT GGC G	L AAT AAT N GAC GAT D GGC GGT G	R CTG CTG L TCC AGC GAC GAC D	D GGT GGT TTC TTT F GAG GAA E	S CAA CAG Q GGT GGC G AAG AAA K	M TTC TTT F GGC GGT G ACC ACC T	Y ATG ATG M ATC ATT I TAT TAT Y	F TAT TAT Y AGG CGC R CTG CTG L
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original	121 421 421 141 481 481 161 541 541 181 601	A AAC AAC N TAC TAT Y AAA AAA AAA K CAA	A CCC CCG P GAC GAT D TCG AGT S GCC	K GCG GCA A GCA A GCA A GCC GCC A TTC	D GTC GTG V ATT ATT I ATT ATG ATG M GCC	S AGC AGT S TTC TTC F AAG AAA K ACT	V CAA CAG Q ATG ATG ATG AAT AAC AAT N GCG	F GGT GGT CAC CAC CAC H GCG GCC A CGG	L AAG AAA K GGC GGC G AAG AAA K AAAG	K TCG AGT S CCC CCG P ACA ACC T AAA	E GAC GAT D GGC GGC GGC CCG CCG P ATC	Q GGA GGT GAC GAC GAC GCC A ATG	D TTG CTG L TCA AGC S CAG CAG CAG Q AAG	K AGC AGT S TCC AGT GGT GGC G CAA	L AAT AAT AAT GAC GAC GGT GGC GGT GAA	R CTG CTG L TCC AGC GAC GAC GAC D AAT	D GGT GGT TTC TTT F GAG GAA E GCA	S CAA CAG Q GGT GGC G AAG AAA K CAT	M TTC TTT F GGC GGT G ACC ACC T TCA	Y ATG ATG ATG ATC ATT I TAT TAT Y GAT	F TAT TAT Y AGG CGC R CTG CTG CTG L ACT
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized	121 421 421 141 481 481 161 541 541 181 601 601	A AAC AAC N TAC TAT Y AAA AAA K CAA	A CCCC CCG P GAC GAT D TCG AGT S GCC GCA	K GCG GCA A GCA GCA GCC GCC A TTC TTT	D GTC GTG V ATT ATT I ATT ATG ATG M GCC GCA	S AGC AGT S TTC TTC TTC F AAG AAA K ACT ACC	V CAA CAG Q ATG ATG ATG ATG AAT N GCG GCA	F GGT GGT CAC CAC CAC CAC H GCG GCC A CGG CGC	L AAG AAA K GGC GGC GGC G AAG AAA K AAG	K TCG AGT S CCCC CCG P ACA ACC T AAA AAG	E GAC GAT D GGC GGC GGC CCG CCG P ATC ATT	Q GGA GGT GAC GAC GAT D GCG GCC A TG ATG	D TTG CTG L TCA AGC S CAG CAG Q AAG AAA	K AGC AGT S TCC AGT GGC GGC G CAA CAG	L AAT AAT AAT GAC GAT GGC GGT GGC GAA GAA	R CTG CTG L TCC AGC GAC GAC GAC D AAT	D GGT GGT TTC TTT F GAG GAA E GCA GCA	S CAA CAG Q GGT GGC GGC AAAG AAA K CAT CAC	M TTC TTT F GGC GGT G ACC ACC T TCA AGT	Y ATG ATG ATG ATG ATT I TAT TAT Y GAT GAT	F TAT TAT Y AGG CGC R CTG CTG CTG L ACT ACC
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid	121 421 421 141 481 481 161 541 541 181 601 601 201	A AAC AAC N TAC TAC TAT Y AAA AAA K CAA CAG Q	A CCCC CCG P GAC GAT D TCG AGT S GCCC GCA A	K GCG GCA A GCA A GCA GCC GCC A TTC TTT F	D GTC GTG V ATT ATT I ATT ATG ATG GCC GCA A	S AGC AGT S TTC TTC F AAG AAA K ACT ACC T	V CAA CAG Q ATG ATG ATG AAT AAC AAT N GCG GCA A	F GGT GGT CAC CAC CAC H GCG GCC A CGG CGC R	L AAG AAA K GGC GGC G AAG AAA K AAG AAA K	K TCG AGT S CCC CCG P ACA ACC T AAA AAG K	E GAC GAT D GGC GGC GGC CCG CCG P ATC ATT I	Q GGA GGT GAC GAC GAC GCC A ATG ATG	D TTG CTG L TCA AGC S CAG CAG CAG Q AAAG AAA K	K AGC AGT S TCC AGT S GGT GGC G CAA CAG Q	L AAT AAT AAT GAC GAT D GGC GGT GAA GAA GAA E	R CTG CTG L TCC AGC GAC GAC D AAT AAT	D GGT GGT TTC TTT F GAG GAA E GCA GCA A	S CAA CAG Q GGT GGC G AAG AAA K CAT CAC H	M TTC TTT F GGC GGT G ACC ACC T TCA AGT S	Y ATG ATG ATG ATG TT TAT TAT TAT TAT Y GAT GAT D	F TAT TAT Y AGG CGC R CTG CTG CTG L ACT ACC T
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original	121 421 421 141 481 481 161 541 541 181 601 601 201 661	A AAC AAC N TAC TAT Y AAA AAA K CAA CAA Q TCA	A CCCC CCG P GAC GAT D TCG AGT S GCCC GCA A CGC	K GCG GCA A GCA A GCC GCC A TTC TTT F GTG	D GTC GTG V ATT ATT ATT ATG ATG GCC GCA A GAC	S AGC AGT S TTC TTC F AAG AAA K ACT ACC T GAC	V CAA CAG Q ATG ATG ATG AAT AAT N GCG GCA A GCG	F GGT GGT G CAC CAC H GCG GCC A CGG CGC R CAG	L AAG AAA K GGCC GGC GAAG AAA K AAAG AAA K CTA	K TCG AGT S CCCC CCG P ACA ACC T AAAA AAG K AAG	E GAC GAT D GGC GGC GGC CCG CCG P ATC ATT I TTC	Q GGA GGT G GAC GAT D GCC GCC A ATG ATG M CTC	D TTG CTG L TCA AGC S CAG CAG CAG CAG AAA AAA K AAC	K AGC AGT S TCC AGT S GGT GGC GGC GGC CAA CAG Q GAA	L AAT AAT N GAC GAT D GGC GGT GAA GAA E GGC	R CTG CTG L TCC AGC GAC GAC GAC GAC D AAT N AAC	D GGT GGT TTC TTT F GAG GAA E GCA GCA A TAC	S CAA CAG Q GGT GGC G G AAG AAA K CAT CAC H GAT	M TTC TTT F GGC GGT G ACC ACC T TCA AGT S CTG	Y ATG ATG M ATC ATT I TAT TAT TAT GAT GAT D CAC	F TAT TAT Y AGG CGC R CTG CTG CTG L ACT ACC T ACA
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized	121 421 421 141 481 481 161 541 541 181 601 601 201 661 661	A AAC AAC N TAC TAT Y AAA AAA K CAA CAG Q TCA AGT	A CCC CCG P GAC GAT D TCG AGT S GCC GCA A CGC CGC	K GCG GCA A GCA GCA A GCC GCC A TTC TTT F GTG GTT	D GTC GTG V ATT ATT I ATT ATG ATG GCC GCA A GAC GAT	S AGC AGT S TTC TTC F AAG AAA K ACT ACC T GAC GAT	V CAA CAG Q ATG ATG ATG AATG M AAC AAT N GCG GCA A GCG GCC	F GGT GGT CAC CAC CAC H GCG GCC A CGG CGC R CAG CAG	L AAAG AAA K GGC GGC GGC GAAG AAAG AAA K AAAG AAA K CTA CTG	K TCG AGT S CCCC CCG P ACA ACC T AAA AAG K AAAG	E GAC GAT D GGC GGC GGC CCG CCG CCG ATT I TTC TTT	Q GGA GGT G GAC GAT D GCG GCC A ATG ATG ATG CTC CTG	D TTG CTG L TCA AGC S CAG CAG CAG CAG AAA K AAAC AAT	K AGC AGT S TCC AGT S GGT GGC GGC CAA CAG Q GAA GAA	L AAT AAT N GAC GAT GGC GGT GAA GAA E GGC GGC	R CTG CTG L TCC AGC GAC GAC GAC D AAT AAT N AAC	D GGT GGT TTC TTT F GAG GAA E GCA GCA A TAC TAT	S CAA CAG Q GGT GGC G AAG AAA K CAT CAC H GAT	M TTC TTT F GGC GGT G GC ACC ACC ACC ACC T TCA AGT S CTG CTG	Y ATG ATG M ATC ATT I TAT TAT TAT GAT GAT D CAC CAT	F TAT TAT TAT Y AGG CGC R CTG CTG CTG L ACT ACC T ACA ACC
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid	121 421 421 141 481 481 161 541 541 541 181 601 601 201 661 661 221	A AAC AAC N TAC TAT Y AAA AAA K CAA CAA CAA CAG CAG S	A CCC P GAC GAT D TCG AGT S GCC GCA A CGC CGC R	K GCG GCA GCA GCA GCC GCC A TTC TTT F GTG GTT V	D GTC GTG V ATT ATT I ATG ATG ATG GCC GCA GAC GAT D	S AGC AGT S TTC TTC F AAG AAA K ACT ACC T GAC GAT D	V CAA CAG Q ATG ATG ATG AATG AATC AAT SCG GCA A GCG GCC A	F GGT GGT CAC CAC CAC H GCG GCC A CGG CGC R CAG CAG Q	L AAG AAA K GGC GGC GGC GAAG AAA K AAA K CTA CTG L	K TCG AGT S CCC CCG P ACA ACC T AAA AAG K AAA K	E GAC GAT D GGC GGC GGC CCG P ATC ATT I TTC TTT F	Q GGA GGT GAC GAC GAC GCC A ATG ATG ATG CTC CTG L	D TTG CTG L TCA AGC S CAG CAG CAG CAG CAG AAA K AAA K AAA N	K AGC AGT S TCC AGT S GGT GGC G CAA CAG Q GAA GAA E	L AAT AAT N GAC GAT D GGC GGT GAA GAA E GGC GGC GGC GGC	R CTG CTG L TCC AGC S GAC GAC GAC D AAT AAT N AAC	D GGT GGT TTC TTT F GAG GCA GCA GCA A TAC TAT Y	S CAA CAG Q GGT GGC G AAG AAA K CAT CAC H GAT GAT D	M TTC TTT F GGC GGT G ACC ACC T CA AGT S CTG CTG L	Y ATG ATG ATG ATG ATG TAT TAT TAT TAT TAT	F TAT TAT Y AGG CGC R CTG CTG CTG CTG L ACT ACC T ACC T
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original	121 421 421 441 481 481 161 541 541 541 181 601 601 201 661 201 661 221 721	A AAC AAC N TAC TAT Y AAA AAA K CAA CAA CAG CAG S CCA	A CCCC P GAC GAT D TCG AGT S GCC GCA A CGC CGC R TTG	K GCG GCA A GCA GCA GCC GCC A TTC TTT F GTG GTT V AAG	D GTC GTG V ATT ATT I ATT ATG ATG GCC GCA GAC GAT D TGG	S AGC AGT S TTC F AAG AAA ACT ACC T GAC GAT D AAG	V CAA CAG Q ATG ATG ATG AAT AAC AAT N GCG GCC A GCC A GCC A GCC	F GGT GGT G CAC CAC H GCG GCC A CGG CGC R CAG CAG CAG Q TAC	L AAAG AAAA K GGCC GGC G AAAG AAAG AAAA K CTA CTG L GGA	K TCG AGT S CCC P ACA ACA AACA AAA AAA K AAA K GAC	E GAC GAT D GGC GGC CCG CCG CCG ATC ATC TTC TTC TTT F CCG	Q GGA GGT GAC GAT D GCG GCC A ATG ATG ATG CTC CTG L TAC	D TTG CTG L TCA AGC S CAG CAG CAG CAG AAA K AAA K AAA K AAA N GAG	K AGC AGT S TCC AGT S GGT GGC G CAA CAA CAA GAA E ATC	L AAT AAT N GAC GAT D GGC GGT GAA GAA E GGC GGC GGC G C AAG	R CTG CTG L TCC AGC GAC GAC GAC GAC D AAT N AAC AAT N	D GGT GGT TTC TTT F GAG GAA E GCA GCA A TAC TAT Y	S CAA CAG Q GGT GGC G AAG AAA K CAT CAC H GAT GAT D	M TTC TTT F GGC GGT G ACC ACC ACC ACC T TCA AGT S CTG CTG L	Y ATG ATG M ATC ATT I TAT TAT TAT GAT GAT D CAC CAT H	F TAT TAT Y AGG CGC R CTG CTG CTG CTG L ACT ACC T ACC T
Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized Amino acid Original Optimized	121   121   421   141   481   481   541   541   601   201   661   221   721   721	A AAC AAC N TAC TAT Y AAA AAA K CAA CAG Q TCA AGT S CCA CCG	A CCCC CCG P GAC GAT D TCG AGT S GCC GCA A CGC CGC R TTG CTG	K GCG GCA A GCA GCA A GCC GCC A TTC TTT F GTG GTT V AAG AAA	D GTC GTG ATT ATT ATT ATT ATT ATG ATG GCC GCA A GAC GAT D TGG TGG	S AGC AGT S TTC F AAG AAG AAG AAC GAC GAC GAC GAA AAA	V CAA CAG Q ATG ATG M AAT M AAC AAT N GCG GCC A GCC A GTC GTT	F GGT GGT CAC CAC H GCG GCC A CGG CAG CAG CAG CAG Q TAC TAT	L AAAG AAAA K GGCC GGC G AAAG AAAA K AAAG AAAA K CTAA CTG L GGA GGT	K TCG AGT S CCC CCG P ACA ACC T AAA AAC T AAA AAG K AAA K GAC GAC	E GAC GAT D GGC GGC CCG CCG P ATC ATT I TTC TTT F CCG CCG	Q GGA GGT G GAC GAT D GCG GCC A ATG ATG ATG CTC CTG L TAC TAT	D TTG CTG L TCA AGC S CAG CAG CAG Q AAG AAA K AAAC AAAT N GAG GAA	K AGC AGT S TCC AGT GGC G CAA CAG GAA GAA E ATC ATT	L AAT AAT N GAC GAT D GGC GGC GGA GGA GAA E GGC GGC GGC G AAG AAG	R CTG CTG L TCC S GAC GAC GAC D AAT N AAT N AAC	D GGT GGT TTC TTT F GAG GAA E GCA GCA A TAC TAT Y	S CAA CAG Q GGT GGC G AAG AAA K CAT CAC H GAT GAT D	M M TTC TTT F GGC GGT G ACC ACC T TCA AGT S CTG CTG L	Y ATG ATG M ATC ATT I TAT TAT TAT Y GAT GAT D CAC CAT H	F TAT TAT Y AGG CGC R CTG CTG CTG L ACT ACC T ACC T

**Figure 3.** The original *csnY* sequence and the optimized sequence based on *E. coli* without signal sequence or stop codon. The mutated codons were highlighted in red; the deduced amino acid sequence was displayed below.



**Figure 4.** SDS-PAGE analysis of recombinant chitosanase CsnY. Lane M: standard Mw markers; lane 1: purified CsnY.

# 2.3. Effects of Temperature and pH on CsnY Activity and Stability

The pH stability of chitosanase CsnY was assessed by the measurement of residual enzymatic activity after incubation at various pH values for 24 h at 4 °C. CsnY kept stable at the range of pH 5.0–9.0, but lost its most of activity when the pH values were out of this range (Figure 5a). Figure 5b indicated that the optimum pH of CsnY was 6.0 in the phosphate buffer and the enzyme maintained relatively high activity between pH 5.0 and 8.0.

Thermal stability of CsnY was analyzed after incubation of enzyme for 0.5 h and 1 h under a variety of temperatures; the results illustrated CsnY possessed favorable thermostability below 50 °C and remained above 80% activity after incubation for 1 h (Figure 5c). As shown in Figure 5d, CsnY had an optimal temperature at 40 °C and contained over 80% activity in the range of 20–50 °C, especially at low temperatures (20–30 °C), demonstrating the cold-adapted property. Noticeably, about 60% activity was maintained even if the temperature was as low as 10 °C (Figure 5d). Furthermore, the thermal stability of CsnY within 12 h was also determined and the results were shown in Figure S1. Although CsnY displayed the optimum activity at 40 °C, it seemed the thermostability of which could not sustain for longer time. The half-life at this temperature was less than 3 h, and almost all the activity was lost after 6 h (Figure S1). However, the thermostabilities were quite better at 20 and 30 °C, the half-lives of CsnY at these temperatures were estimated to be over 6 and 4 h, respectively, and 30.2% and 21.3% relative activities were remained even after 12 h (Figure S1), indicating the industrial availability of CsnY at room temperature.



(c)

(**d**)

**Figure 5.** Effects of pH and temperature on the activity and stability of CsnY. (**a**) The pH stability of CsnY was analyzed after incubation for 24 h in the pH range of 3.5 to 10.0, with the sodium acetate-acetic acid buffer (pH 3.5–5.5), Na<sub>2</sub>HPO<sub>4</sub>– NaH<sub>2</sub>PO<sub>4</sub> buffer (pH 5.5–8.0), Tris–HCl buffer (7.0–8.5), and Gly–NaOH buffer (pH 8.5–10.0), the highest residual activity was taken as 100%; (**b**) the optimum pH of CsnY was determined in the pH range of 3.5 to 10.0 with the buffers above by setting the activity at the optimal pH as 100%; (**c**) the temperature stability of CsnY was assessed by analyzing the residual activity of CsnY after incubation under 0–70 °C for 0.5 and 1 h, with the initial activity as 100%; (**d**) the optimal temperature of CsnY was determined at the range of 0–80 °C, taking the activity at the optimum temperature as 100%.

# 2.4. The Effects of Various Metal Ions or Chemicals on CsnY

In order to investigate the effects on CsnY activity of various metal ions and chemicals, the retained activities were monitored in the presence of these substances with the concentration of 1 mM. Figure 6 showed that the activity of CsnY had a 2.78-fold increase when  $Mn^{2+}$  was added into the reaction system. On the contrary, Co<sup>2+</sup> had an obvious inhibitory influence on the activity of CsnY and resulted in over 35% loss of enzyme activity (Figure 6).

## 2.5. Final Degradation Product Analysis

Considering the effect on enzymatic reaction brought by high viscosity of polysaccharides, 2% (w/v) chitosan solution was used as the substrate. The depolymerization reaction was performed at room temperature (approximately 25 °C) by using cold-adapted CsnY, and the amount of reducing sugar in the reaction mixture was determined periodically. After hydrolysis for 1 h, the increase in reducing sugar became painfully slow, and finally, the concentration of which was determined as 56.74 mM at 2 h (Figure S2). Thin-layer chromatography (TLC) and positive-ion electrospray ionization mass spectrometry (ESI-MS) were applied to analyze the final hydrolysis products, and the results were displayed in Figure 7. At the end of the reaction, two clear spots corresponding to chitobiose and -triose, respectively, of markers were clearly observed on the TLC plate (Figure 7a). Therefore, the final depolymerization products of CsnY towards chitosan contained chitotrisaccharide and -disaccharide. As shown in Figure 7b, two main ion peaks with the mass-to-charge ratios (m/z) of 341.3 and 502.3 appeared under the positive mode, corresponding to [DP2 + H]<sup>+</sup> and [DP3+H]<sup>+</sup>, respectively, and the peak of 363.3 m/z presumably belonged to [DP2 + Na]<sup>+</sup>. Therefore, disaccharinde and trisaccharide were proven to be the main products in accordance with the TLC analysis result. Interestingly, almost all of the chitosan substrates were degraded by CsnY, and no oligosaccharide with DP > 3 was detected by both TLC and ESI-MS methods (Figure 7). Moreover, the releasing mode of products and the rapid decrease in the viscosity of the mixture (data not shown) suggested that the chitosanase CsnY was active in an endolytic manner.



Figure 6. Effects of different metal ions or chemicals on the enzymatic activity of CsnY.



**Figure 7.** Hydrolysis product analysis by TLC and ESI-MS. (a) TLC analysis of end product. Lane M: a mixture of chitomonomer (DP1), -dimer (DP2), and -trimer (DP3); lane 1: mixture before reaction; lane 2: reaction products of CsnY. (b) ESI-MS analysis of degraded products.

# 3. Discussion

Sequence analysis result revealed that several essential amino acid residues existed in CsnY and were marked by green star in Figure 2, among which two highly conserved residues (Glu<sup>98</sup> and Asp<sup>116</sup>) were required for catalysis. Owing to the previous research, during the hydrolysis process, the Glu protonated the glycosidic oxygen and the Asp polarized the attacking water in the inverting catalytic reaction [20,21]. Experimentally confirmed by Lacombe-Harvey et al., Asp<sup>116</sup>, Arg<sup>118</sup> and Thr<sup>121</sup> residues were strictly conserved in chitosanases and essential for catalysis [22]. Additionally, other several residues as the members of ionic interaction network, including Asp<sup>222</sup>, Arg<sup>267</sup> and Arg<sup>282</sup>, could stabilize the catalytic cleft with each other [21].

The biochemical properties of recombinant CsnY were surveyed. CsnY had a stable activity at the range of pH 5.0–9.0 (Figure 5a), which was similar with that of other bacterial chitosanases, such as Csn21c, CsnM, and CsnQ, displayed a stable activity when the pH values were from 4.0 to 9.0 [16,23,24]. The chitosanase isolated from *Renibacterium* sp. QD1 maintained stable at pH 5–10 where more than 90% of original activity was retained [12]. The optimum pH of the chitosanase CsnY was determined as 6.0 (Figure 5b). As previously reported, the optimal pH values for most of chitosanases were located at acidic or neutral range (pH 4–7) [23,25]. For example, the chitosanase Csna expressed the highest activity at the range of pH 5.3–6.0, and some other chitosanases, such as BaCsn46B and the chitosanase from *Paenibacillus mucilaginusus* TKU032, displayed the analogous optimum pH values as Csna [1,26].

The optimum temperature of cold-adapted CsnY was 40 °C (Figure 5d). The optimal temperatures of cold-adapted enzymes are generally below 35 °C [17–19]. Previous reports showed that the cold-adapted chitosanases GsCsn46A and Csn-CAP displayed the maximum activity at 30 °C [27,28]. However, some other chitosanases with cold-adapted property had the highest activity at the temperatures above 35 °C (Table 1).

Name/Source	Mw (kDa)	Optimum pH/Temperature (°C)	Specific Activity (U/mg)	Relative Activity at 10/20/30 °C	Thermal Stability	Final Products	Reference
CsnY/ <i>Renibacterium</i> sp. Y82	27.8	6.0/40	330.67	60%/80%/>80%	80% activity remained after 1 h at 50 °C	DP2,3	This study
CsnB/Bacillus sp. BY01	30.89	5.0/35	329.3	40.4%/76.8%/>80%	10% activity retained after 1 h at 40 °C	DP2,3	[15]
CsnM/Pseudoalteromonas sp. SY39	28	5.9/40	393.2	30.6%/>50%/80%	15.8% activity retained at 30 and 40 °C for 1 h	DP2,3	[16]
Csn-CAP/Staphylococcus capitis	35	7.0/30	89.2	N.D./90%/90%	50% activity retained at 55 °C for 1 h	DP2,3	[27]
GsCsn46A/Gynuella sunshinyii	29.7	5.5/30	260.39	70%/>80%/>80%	80% activity remained at 30 °C for 1 h	DP2,3	[28]
CsnS/Serratia sp. QD07	27.1	5.8/60	412.6	42.6%/40%/>40%	retained at 30 °C for 2 h	DP2,3	[29]
N.D./Janthinobacterium sp. 4239	29	5.0/45	1500	30%/60%/70%	almost all the activity retained after 30 min at 50 °C	DP1-3	[30]

Table 1. Comparison of the properties among CsnY and other cold-adapted chitosanases.

Similar to CsnY, CsnM also showed the optimal activity at 40 °C [16]. Interestingly, CsnY possessed wider temperature range for the activity compared with other chitosanases (see Table 1 for details), with relatively high activity (over 80%) at the temperatures ranging

from 20 to 50 °C, especially at low temperatures (20–30 °C) (Figure 5d). Noticeably, about 60% activity was maintained even if the temperature was as low as  $10 \degree C$  (Figure 5d), which is rare among all the reported chitosanases. As the cold-adapted chitosanases, CsnS and CsnB retained 42.6% and 40.4% of its maximum activity, respectively, at 10 °C [15,29], GsCsn46A maintained 70% of its initial activity but with worse thermostability and lower specific activity compared with CsnY [28]. These results demonstrated that CsnY had an excellent cold-adapted property, which could be used at room temperature (generally 25 °C) or even lower temperatures to run biocatalytic processes without heating, in order to save energy and production costs, and to reduce contamination risks [16]. Although sharing the same optimal temperature with some other cold-adapted chitosanases (such as CsnM, CsnB, and the chitosanase from Janthinobacterium sp. 4239), CsnY exhibited much higher relative activity than those enzymes under 10 to 30  $^{\circ}$ C (Table 1), signifying better cold-adapted property owned by CsnY, which revealed a superior potential for application to prepare COS at room temperature. The chitosanases properties have a close relationship with the growth conditions of the microorganisms which produce chitosanases; the temperatures of the marine environments are generally relatively low, and thus the enzymes derived from marine microorganisms such as CsnY often possess particular properties such as cold adaptation, helping these microorganisms better adapt to outside environments [31]. Cold-adapted enzymes usually have a higher degree of flexibility, particularly in the region of active sites [19]. Their catalysis reactions invariably show smaller enthalpy and more negative entropy of activation, the reduction in the activation enthalpy weakens the temperature dependence of the reaction rate, which thus facilitates catalysis at low temperature [19]. Therefore, the chitosanase CsnY with the cold-adapted property may be relevant with protein flexibility, and perhaps another work related to the three-dimensional structure of CsnY will be carried out in the future to further elucidate why it possesses such excellent cold-adapted properties.

In addition, the CsnY exhibited higher thermostability than other cold-adapted chitosanases over a broad temperature range of 0 to 50 °C (see Table 1 for details). Due to catalysis reactions conducted by cold-adapted enzymes usually at low temperatures (20–30 °C), they are supposed to have lower thermostability than their mesophilic homologs, rapid deactivation occurs even when the environmental temperature increases slightly [15,18,19]. However, CsnY showed thermo-stable property and industrial availability within at least 12 h (Figure S1), which is beneficial for extended use, storage, and transport of the enzyme.

The activity of CsnY could be significantly enhanced by  $Mn^{2+}$  but inhibited by  $Co^{2+}$  (Figure 6). For some chitosanases, such as CsnB, Csn-CAP, CSN, and CsnW2,  $Mn^{2+}$  has obviously enhanced their enzymatic activities, with an increase of 2.57, 1.89, 1.9, and 1.16-fold, respectively [15,27,32,33]. The increases in chitosanase enzymatic activities can be explained that  $Mn^{2+}$  favors the saccharification process resulting in higher production of reducing sugars, GH-46 family chitosanases have the metal ion binding sites where some metal ions such as  $Mn^{2+}$  may bind to these sites and thus, helpful to enhance the three-dimensional structural stabilities, and catalytic activities of chitosanases [15]. Similar with CsnY,  $Co^{2+}$  also had an inhibitory impact on CsnM [16]. Surprisingly, distinguished from other chitosanases, no obvious enzyme activity changes were observed when other kinds of metal ions or chemical reagents, including Fe<sup>3+</sup>, Cu<sup>2+</sup>, EDTA, and SDS, were added into the reaction systems (Figure 6). The results above illustrated that CsnY could still keep a high stability under the influence of different metal ions and chelators, and had a desirable potential for industrial application.

CsnY degraded 2% (w/v) chitosan efficiently and thoroughly within 2 h releasing chitodisaccharides and -trisaccharides as main products with the total concentration of 56.74 mM (Figure S2 and Figure 7), almost all of the substrates were degraded by CsnY within 2 h, and no oligosaccharide with DP > 3 was found by both TLC and ESI-MS methods (Figure 7), demonstrating the strongly depolymerized ability of CsnY against chitosan, which benefited from favorable catalytic activity. The specific activity of CsnY

was determined as 330.67 U/mg, although this activity was detected not under the optimal condition, which was relatively high among cold-adapted chitosanases (Table 1), and able to satisfy the application in the industrial preparation of COS. Obviously, more chitosan could be used during COS production by CsnY, but the influence on enzymatic hydrolysis brought by high viscosity of polysaccharides appeared when increasing the concentration of substrate. Fortunately, CsnY could at least retain its stability at room temperatures (20-30 °C) for a longer time (Figure S1). Therefore, maybe it would be better adding the chitosan substrate in batches. The systematic research of COS preparation by CsnY will be performed in another work. Similarly, previous research showed that a number of cold-adapted chitosanases, which were determined as endo-type enzymes, catalyzed the cleavage of  $\beta$ -1,4-glycosidic linkage and released chitobiose and -triose (Table 1). During the enzymatic production of COS, simple product distribution would be significant for the following separation and purification. Some chitosanases reported previously degraded substrate with mixed COS of DP2–5 as the final products [32,34,35], thus compounding the difficulty for separation. However, although many cold-adapted chitosanases shared the same final products to CsnY, the production efficiency of them were far less [15,16], especially for CsnM, which thoroughly degraded chitosan substrate until 24 h later at 30 °C [16]. The high degradation specificity of CsnY is propitious to high-efficiency production of COS, combined with the desirable cold adaptation, favorable stability, strong resistance to most ions and chemicals; all of these outstanding properties suggest CsnY would be a potent tool for industrial production.

## 4. Materials and Methods

#### 4.1. Materials, Strains, Plasmids, and Media

Chitosan (viscosity: 200 mPa·s; deacetylation degree: 95%) was purchased from Aladdin Biochemical Technology Co., Ltd. (Shanghai, China). Standard chitosan trisaccharide, disaccharide, and monosaccharide were purchased from Qingdao BZ Oligo Biotech Co., Ltd. (Qingdao, China). The TLC silica gel plates 60 F254 were bought from Merck KGaA (Darmstadt, Germany).

The marine bacterium strain *Renibacterium* sp. Y82 was isolated from brown seaweed in the Yellow Sea, China. In brief, the chips of rotten brown seaweed were put into the chitosan sole-carbon medium. After culture in the flask for microorganism enrichment and spread plate cultivation for isolation, a *Renibacterium* sp. strain named Y82 was found to grow in the chitosan sole-carbon medium, signifying the ability to degrade and apply chitosan (detailed data not shown), and stored in the laboratory. *E. coli* DH5 $\alpha$  and BL21 (DE3) were used for plasmid construction and *csnY* gene expression, respectively. Both these strains were cultured at 37 °C in Luria-Bertani (LB) broth or solid medium with 2% (*w*/*v*) agar, into which 50 µg/mL kanamycin was supplemented if necessary. Expression vector pET-28a (+) was purchased from Novagen (Madison, WI, USA).

#### 4.2. Sequence Analysis of CsnY

Based on the genomic analysis of *Renibacterium* sp. Y82 (relevant data not published), a putative gene named *csnY* which encoding a chitosanase CsnY was found and deposited in the Genbank getting the accession number MT741946, 22 May 2021. The conserved domain and the signal peptide of CsnY were analyzed by the Conserved Domain Database (CDD) (https://www.ncbi.nlm.nih.gov/cdd) and SignalP 5.0 server (http://www.cbs.dtu.dk/services/SignalP/) [36], respectively. The theoretical pI and Mw of CsnY were calculated using the compute pI/Mw Tool (https://web.expasy.org/ compute\_pi/). To clarify the evolutionary relationship among CsnY and other chitosanases from bacteria, the phylogenetic tree construction was executed by the neighbor-joining method with MEGA 6.0 software, according to the protein sequences of related chitosanases obtained from National Center of Biotechnology Information (NCBI), Bethesda, MD, USA (https://www.ncbi.nlm.nih.gov/) [37]. The multiple sequences alignment was created by means of DNAMAN software (Lynnon Biosoft, Foster City, CA, USA) [38].

#### 4.3. Codon Optimization and Construction of Expression Vector

Following elimination of the rare codons used in *E. coli* and addition of *NcoI* and *XhoI* restriction sites to the terminals (Figure 3), the *csnY* gene (762bp, see Figure 3 for detailed sequence) without signal sequence and stop codon was synthesized by Synbio Technologies LLC (Synbio Technologies, Suzhou, China). The synthesized DNA was digested through restriction endonucleases *NcoI* and *XhoI*, afterwards, the digested *csnY* gene fragment was purified and ligated into the corresponding sites of the plasmid pET-28a (+) using T4 DNA ligase to construct the final recombinant plasmid with a C-terminal  $6 \times$ His-tag, which was then transformed into *E. coli* BL21 (DE3) cells for enzyme expression.

#### 4.4. Expression and Purification of CsnY

The recombinant *E. coli* BL21 (DE3) harboring the csnY gene was cultured in the LB broth supplemented with 50  $\mu$ g/mL kanamycin at 37 °C till OD<sub>600nm</sub> reached around 0.8. CsnY induction expression was carried out by using 0.5 mM IPTG for 20 h at 16 °C and 180 rpm. Cells were collected via centrifugation and suspended in 50 mM phosphate buffer (pH 7.0), and then sonicated at 4 °C. The crude protein supernatant obtained through centrifugation was injected into the Ni-NTA agarose column (TaKaRa, Dalian, China) which was already equilibrated by 50 mM phosphate buffer (pH 7.0) containing 300 mM NaCl and 15 mM imidazole. The column was then successively subjected to the same buffer with 30 mM imidazole to wash the sample and remove protein impurities, and to the same buffer with a linear gradient of imidazole (50-400 mM) to elute the 6×His-tagged CsnY. The eluted fractions with chitosanase activity were collected and pooled, then concentrated with a Millipore centrifugal filter 3 K device (Millipore, Burlington, MA, USA), meanwhile, the enzyme solution was desalted and 50 mM Tris-HCl (pH 7.0) was employed to replace the phosphate buffer. 12% of SDS-PAGE system (Bio-Rad, Hercules, CA, USA) was applied to analyze the Mw of recombinant CsnY, the loading amount was set as 10  $\mu$ L. The protein marker was bought from Solarbio Life Sciences (Beijing, China). BCA protein assay kit (Solarbio, Beijing, China) was used to measure the total protein concentration.

## 4.5. Measurement of CsnY Activity

The chitosanase activity was detected at 40 °C and pH 7.0 according to the description by Zhou et al. [16]. In brief, enzymatic reaction was performed with 100  $\mu$ L properly diluted CsnY solution and 900  $\mu$ L substrate solution of 0.3% (w/v) chitosan for 10 min. Then, the reducing sugars were determined using 3,5-dinitrosalicylic acid (DNS) method [39]. One unit of chitosanase was defined as the amount of enzyme that generated reducing sugars corresponding to 1  $\mu$ mol of glucosamine hydrochloride per min.

#### 4.6. Effects of Temperature and pH on CsnY Activity and Stability

A total amount of 20 mM of four different buffers, including NaAc-HAc (pH 3.5–5.5), phosphate buffer (pH 5.5–8.0), Tris-HCl (pH 7.0–8.5), and Gly-NaOH (8.5–10.0), were used to evaluated pH stability of CsnY by measuring the residual enzymatic activities after incubation at 4 °C for 24 h, here taking the highest residual activity as 100%. To determine the optimum pH of CsnY, the enzymatic activities were measured in the four different buffers (pH 3.5–10.0) mentioned above at 40 °C by taking the activity at optimal pH as 100%. Thermostability of CsnY was assessed over the range of 0–70 °C, residual enzyme activities were detected after 0.5 and 1 h of incubation and calculated with the initial activity as 100%. The optimal temperature of the purified enzyme was determined over the range of 0–80 °C by setting the activity at the optimum temperature as 100%.

In order to assess the ability of CsnY for catalytic hydrolysis in a longer time, the thermal stabilities of CsnY within 12 h was investigated on the basis of the residual activities of CsnY measured at various time intervals during incubation at certain temperatures (20  $^{\circ}$ C, 30  $^{\circ}$ C, and 40  $^{\circ}$ C).

#### 4.7. The Effects of Various Metal Ions or Chemicals on CsnY Activity

Different kinds of metal salts and chemical reagents with the concentration of 1 mM were added into the standard reaction solution to investigate their effects on CsnY activity. The relative activities were calculated with respect to the control sample where the reaction was conducted in the absence of any additive.

#### 4.8. Analysis of Degradation Products

For enzymatic product analysis, 2% (w/v) chitosan solution as the substrate, was mixed with excess CsnY (10 U per mg of chitosan). The mixture was continuously stirred at room temperature (approximately 25 °C) to guarantee the depolymerization reaction was performed. Reducing sugar content in the reaction mixture was detected periodically by DNS method [39], to certify the degradation products no longer changed. Then, the mixture solution was concentrated using a centrifugal filter 3 K device (Millipore, Burlington, MA, USA), meanwhile, the proteins and undegraded macromolecules were removed. The end product of CsnY against chitosan was analyzed by means of TLC, following the previously described method [16,40]. Briefly, the samples on the plate were developed with a mixture of ammonia, water, and isopropanol (3:27:70, v/v/v) as the developing solvent, and visualized after drying the plate by spraying with 0.5% (w/v) ninhydrin in ethanol, and heating at 80 °C for 20 min. To further investigate the DPs of the oligosaccharides in the final product, the product solution was mixed with methanol (1:1, v/v), then quantitatively injected into an ESI-MS instrument (Bruker Esquire HCT, Billerica, MA, USA). The hydrolytic products were profiled in positive-ion mode under the following conditions: calibration dynamics, 2; cone voltage, 20.00 V; capillary voltage, 4.00 kV; desolvation temperature, 350 °C; source temperature, 150 °C; desolvation gas flow, 500 L/h; cone gas flow rate, 50 L/h; scan range, 100–1500 m/z [38].

#### 5. Conclusions

In this work, a novel GH46 family chitosanase CsnY from marine bacterium *Renibacterium* sp. Y82 was heterologously expressed, purified, and characterized. Significantly, CsnY was a cold-adapted enzyme with favorable stability, especially showing high relative activity at low temperature (10–30 °C). Moreover, most metal ions or chemicals had no obvious influence on the enzymatic activity of CsnY, which released chitodisaccharide and -trisaccharide from chitosan. These properties suggest CsnY would be an excellent potential candidate for industrial preparation of COS. The future works will focus on the three-dimensional structure analysis of CsnY to further elucidate the relationship between the structure and its excellent cold-adapted property, and the systematic study of COS preparation by CsnY.

**Supplementary Materials:** The following are available online at https://www.mdpi.com/article/ 10.3390/md19110596/s1. Figure S1: Thermal stability of CsnY within 12 h. Figure S2: Catalytic hydrolysis of chitosan by CsnY.

Author Contributions: Conceptualization, H.-X.Z. and Z.-P.W.; methodology, Z.-P.W.; software, X.-H.J.; validation, X.-F.X.; formal analysis, W.-X.Z.; investigation, Y.-Q.S.; resources, H.-X.Z. and Z.-P.W.; data curation, H.-X.Z. and Z.-P.W.; writing—review and editing, H.-X.Z. and L.-L.Z.; visualization, L.-L.Z.; supervision, H.-X.Z. and Z.-P.W.; project administration, Z.-P.W.; funding acquisition, H.-X.Z. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research was funded by Shandong Provincial Natural Science Foundation, China, grant number ZR2017BC029.

Conflicts of Interest: The authors declare no conflict of interest.

#### References

- Doan, C.T.; Tran, T.N.; Nguyen, V.B.; Nguyen, A.D.; Wang, S.L. Production of a thermostable chitosanase from shrimp heads via *Paenibacillus Mucilaginosus* TKU032 conversion and its application in the preparation of bioactive chitosan oligosaccharides. *Mar. Drugs* 2019, 17, 217. [CrossRef]
- Sanchez, A.; Mengibar, M.; Fernandez, M.; Alemany, S.; Heras, A.; Acosta, N. Influence of preparation methods of chitooligosaccharides on their physicochemical properties and their anti-inflammatory effects in mice and in RAW 264.7 macrophages. *Mar. Drugs* 2018, *16*, 430. [CrossRef]
- Mei, Y.X.; Chen, H.X.; Zhang, J.; Zhang, X.D.; Liang, Y.X. Protective effect of chitooligosaccharides against Cyclophosphamideinduced immunosuppression in mice. *Int. J. Biol. Macromol.* 2013, 62, 330–335. [CrossRef]
- 4. Lin, S.M.; Mao, S.H.; Guan, Y.; Lin, X.; Luo, L. Dietary administration of chitooligosaccharides to enhance growth, innate immune response and disease resistance of *Trachinotus ovatus*. *Fish Shellfish Immun.* **2012**, *32*, 909–913. [CrossRef]
- Inmaculada, A.; Niuris, A.; Concepción, C.; Begoña, E.; Javier, M.; Carolina, C.; María, G.; Angeles, C. Cosmetics and cosmeceutical applications of chitin, chitosan and their derivatives. *Polymers* 2018, 10, 213–238.
- 6. Malerba, M.; Cerana, R. Recent advances of chitosan applications in plants. *Polymers* **2018**, *10*, 118. [CrossRef] [PubMed]
- 7. Schmitz, C.; Auza, L.G.; Koberidze, D.; Rasche, S.; Fischer, R.; Bortesi, L. Conversion of chitin to defined chitosan oligomers: Current status and future prospects. *Mar. Drugs* **2019**, *17*, 452. [CrossRef] [PubMed]
- Jung, W.J.; Park, R.D. Bioproduction of chitooligosaccharides: Present and perspectives. *Mar. Drugs* 2014, 12, 5328–5356. [CrossRef] [PubMed]
- Kim, E.K.; Je, J.Y.; Lee, S.J.; Kim, Y.S.; Hwang, J.W.; Sung, S.H.; Moon, S.H.; Jeon, B.T.; Kim, S.K.; Jeon, Y.J.; et al. Chitooligosaccharides induce apoptosis in human myeloid leukemia HI-60 cells. *Bioorg. Med. Chem. Lett.* 2012, 22, 6136–6138. [CrossRef] [PubMed]
- 10. Viens, P.; Lacombe-Harvey, M.E.; Brzezinski, R. Chitosanases from family 46 of glycoside hydrolases: From proteins to phenotypes. *Mar. Drugs* 2015, *13*, 6566–6587. [CrossRef] [PubMed]
- Zhang, C.; Kim, S.K. Application of marine microbial enzymes in the food and pharmaceutical industries. *Adv. Food. Nutr. Res.* 2012, 65, 423–435. [PubMed]
- 12. Xing, P.C.; Liu, D.; Yu, W.G.; Lu, X.Z. Molecular characterization of an endo-type chitosanase from the fish pathogen *Renibacterium* sp. QD1. *J. Mar. Biol. Assoc. UK* **2014**, *94*, 681–686. [CrossRef]
- 13. Guan, F.; Han, Y.; Yan, K.; Zhang, Y.; Zhang, Z.; Wu, N.; Tian, J. Highly efficient production of chitooligosaccharides by enzymes mined directly from the marine metagenome. *Carbohydr. Polym.* **2020**, 234, 115909. [CrossRef] [PubMed]
- 14. Cavicchioli, R.; Charlton, T.; Ertan, H.; Mohd Omar, S.; Siddiqui, K.S.; Williams, T.J. Biotechnological uses of enzymes from Psychrophiles. *Microb. Biotechnol.* **2011**, *4*, 449–460. [CrossRef] [PubMed]
- 15. Yang, Y.; Zheng, Z.; Xiao, Y.; Zhang, J.; Zhou, Y.; Li, X.; Li, S.; Yu, H. Cloning and characterization of a cold-adapted chitosanase from marine bacterium *Bacillus* sp. BY01. *Molecules* **2019**, *24*, 3915. [CrossRef]
- 16. Zhou, Y.; Chen, X.H.; Li, X.; Han, Y.T.; Wang, Y.A.; Yao, R.Y.; Li, S.Y. Purification and characterization of a new cold-adapted and thermo-tolerant chitosanase from marine bacterium *Pseudoalteromonas* sp. SY39. *Molecules* **2019**, *24*, 183. [CrossRef]
- 17. Siddiqui, K.S.; Cavicchioli, R. Cold-adapted enzymes. Annu. Rev. Biochem. 2006, 75, 403–433. [CrossRef]
- 18. Gerday, C.; Aittaleb, M.; Bentahir, M.; Chessa, J.P.; Claverie, P.; Collins, T.; D'Amico, S.; Dumont, J.; Garsoux, G.; Georlette, D.; et al. Cold-adapted enzymes: From fundamentals to biotechnology. *Trends. Biotechnol.* **2000**, *18*, 103–107. [CrossRef]
- 19. Åqvist, J.; Isaksen, G.V.; Brandsdal, B.O. Computation of enzyme cold adaptation. *Nat. Rev. Chem.* **2017**, *1*, 0051. [CrossRef]
- 20. Shinya, S.; Fukamizo, T. Interaction between chitosan and its related enzymes: A review. *Int. J. Biol. Macromol.* 2017, 104, 1422–1435. [CrossRef]
- Fukamizo, T.; Juffer, A.H.; Vogel, H.J.; Honda, Y.; Tremblay, H.; Boucher, I.; Neugebauer, W.A.; Brzezinski, R. Theoretical calculation of pK<sub>a</sub> reveals an important role of Arg205 in the activity and stability of *Streptomyces* sp. N174 chitosanase. *J. Biol. Chem.* 2000, 275, 25633–25640. [CrossRef]
- 22. Lacombe-Harvey, M.; Fortin, M.; Ohnuma, T.; Fukamizo, T.; Letzel, T.; Brzezinski, R. A highly conserved arginine residue of the chitosanase from *Streptomyces* sp. N174 is involved both in catalysis and substrate binding. *BMC Biochem.* 2013, 14, 23. [CrossRef]
- 23. Guo, N.; Sun, J.A.; Wang, W.; Gao, L.; Mao, X.Z. Cloning, expression and characterization of a novel chitosanase from *Streptomyces albolongus* ATCC 27414. *Food. Chem.* **2019**, *286*, 696–702. [CrossRef]
- Ma, C.R.; Li, X.; Yang, K.; Li, S.Y. Characterization of a new chitosanase from a marine *Bacillus* sp. and the anti-oxidant activity of its hydrolysate. *Mar. Drugs* 2020, 18, 126. [CrossRef]
- Bhuvanachandra, B.; Sivaramakrishna, D.; Alim, S.; Preethiba, G.; Rambabu, S.; Swamy, M.J.; Podile, A.R. New class of chitosanase from *Bacillus amyloliquefaciens* for the generation of chitooligosaccharides. *J. Agric. Food. Chem.* 2021, 69, 78–87. [CrossRef] [PubMed]
- Luo, S.; Qin, Z.; Chen, Q.M.; Fan, L.Q.; Jiang, L.H.; Zhao, L.M. High level production of a *Bacillus amlyoliquefaciens* chitosanase in *Pichia Pastoris* suitable for chitooligosaccharides preparation. *Int. J. Biol. Macromol.* 2020, 149, 1034–1041. [CrossRef]
- 27. Sun, H.H.; Cao, R.; Li, L.H.; Zhao, L.; Qiu, L. Cloning, purification and characterization of a novel GH46 family chitosanase, Csn-CAP, from *Staphylococcus capitis*. *Process. Biochem.* **2018**, 75, 146–151. [CrossRef]
- 28. Wang, Y.N.; Qin, Z.; Fan, L.Q.; Zhao, L.M. Structure–function analysis of *Gynuella sunshinyii* chitosanase uncovers the mechanism of substrate binding in GH family 46 members. *Int. J. Biol. Macromol.* **2020**, *165*, 2038–2048. [CrossRef]

- 29. Zheng, Q.; Meng, X.; Cheng, M.; Li, Y.; Liu, Y.; Chen, X. Cloning and Characterization of a New Chitosanase From a Deep-Sea Bacterium *Serratia* sp. QD07. *Front. Microbiol.* **2021**, *12*, 360. [CrossRef]
- 30. Johnsen, M.G.; Hansen, O.C.; Stougaard, P. Isolation, characterization and heterologous expression of a novel chitosanase from *Janthinobacterium* sp. strain 4239. *Microb. Cell. Fact.* **2010**, *9*, 5. [CrossRef] [PubMed]
- 31. Kaczmarek, M.B.; Struszczyk-Swita, K.; Li, X.; Szczesna-Antczak, M.; Daroch, M. Enzymatic modifications of chitin, chitosan, and chitooligosaccharides. *Front. Bioeng. Biotechnol.* **2019**, *7*, 243. [CrossRef] [PubMed]
- Zhang, J.; Cao, H.; Li, S.; Zhao, Y.; Wang, W.; Xu, Q.; Du, Y.; Yin, H. Characterization of a new family 75 chitosanase from Aspergillus sp. W-2. Int. J. Biol. Macromol. 2015, 81, 362–369. [CrossRef] [PubMed]
- Zhu, X.F.; Tan, H.Q.; Zhu, C.; Liao, L.; Zhang, X.Q.; Wu, M. Cloning and overexpression of a new chitosanase gene from *Penicillium* sp. D-1. *AMB Express* 2012, 2, 13. [CrossRef] [PubMed]
- Goo, B.G.; Park, J.K. Characterization of an alkalophilic extracellular chitosanase from *Bacillus cereus* GU-02. *J. Biosci. Bioeng.* 2014, 117, 684–689. [CrossRef]
- Gao, X.A.; Jung, W.J.; Kuk, J.H.; Park, R.D. Reaction pattern of *Bacillus cereus* D-11 chitosanase on chitooligosaccharide alcohols. *J. Microbiol. Biotechnol.* 2009, 19, 358–361. [CrossRef] [PubMed]
- 36. Zhang, L.L.; Li, J.; Wang, Y.L.; Liu, S.; Wang, Z.P.; Yu, X.J. Integrated approaches to reveal genes crucial for tannin degradation in *Aureobasidium melanogenum* T9. *Biomolecules* **2019**, *9*, 439. [CrossRef]
- 37. Xue, J.L.; Wu, Y.N.; Shi, K.; Xiao, X.F.; Gao, Y.; Li, L.; Qiao, Y.L. Study on the degradation performance and kinetics of immobilized cells in straw-alginate beads in marine environment. *Bioresour. Technol.* **2019**, *280*, 88–94. [CrossRef]
- Zhou, H.X.; Xu, S.S.; Yin, X.J.; Wang, F.L.; Li, Y. Characterization of a new bifunctional and cold-adapted polysaccharide lyase (PL) family 7 alginate lyase from *Flavobacterium* sp. *Mar. Drugs* 2020, *18*, 388. [CrossRef]
- 39. Miller, G.L. Use of dinitrosalicylic acid reagent for determination of reducing sugar. Anal. Chem. 1959, 31, 426–428. [CrossRef]
- 40. Zhang, Y.H.; Shao, Y.; Jiao, C.; Yang, Q.M.; Weng, H.F.; Xiao, A.F. Characterization and application of an alginate lyase, Aly1281 from marine bacterium *Pseudoalteromonas carrageenovora* ASY5. *Mar. Drugs* **2020**, *18*, 95. [CrossRef]